The era of metagenomics to study sponges

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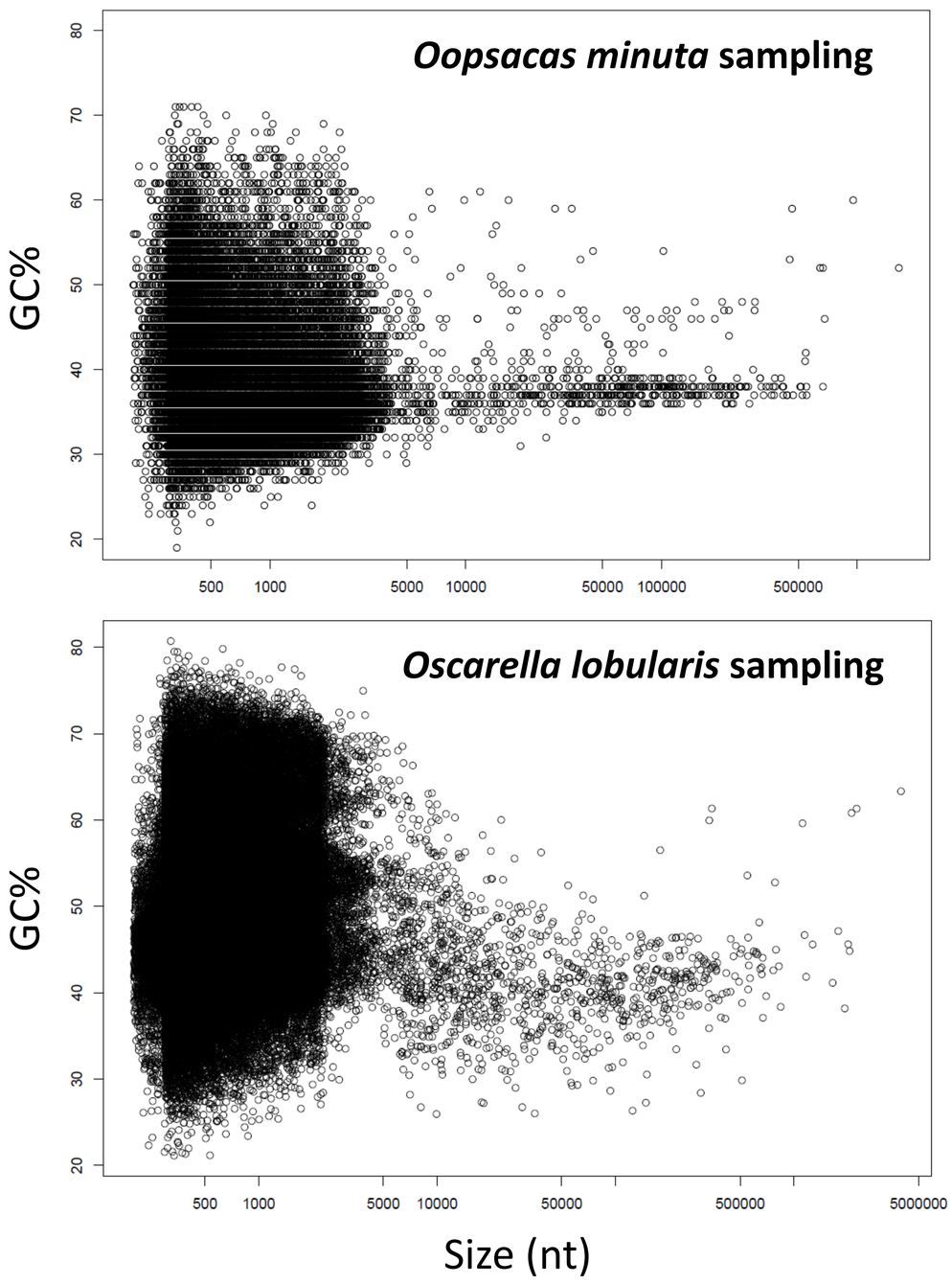
INTRODUCTION

- Genome sequencing and assembly of eukaryota organisms remain challenging.
- Sponges are organisms known to be associated with diverse microorganisms.
- Here, we present an attempt of sequencing of two mediterranean sponges (Porifera):
  Oscarella lobularis (homoscleromorpha) and ***Oopsacas minuta*** (Hexactinellida).

METHOD

1. Sampling organisms as clean as possible
2. DNA extraction
3. Illumina sequencing (Pair-Ends & Mate Pairs)
4. Homemade assembly pipeline (IDBA-UD + Platanus + GapFiller)
5. Metagenome taxonomic assignment (homology-based method)
6. Species relative abundance computation (Bowtie: reads mapping)

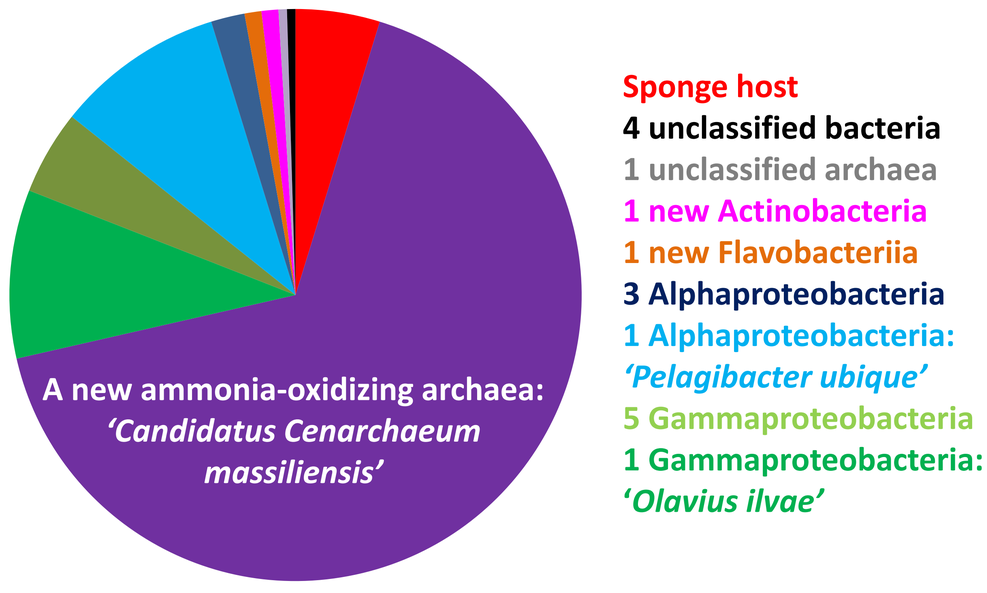
A lot of genomic fragments…



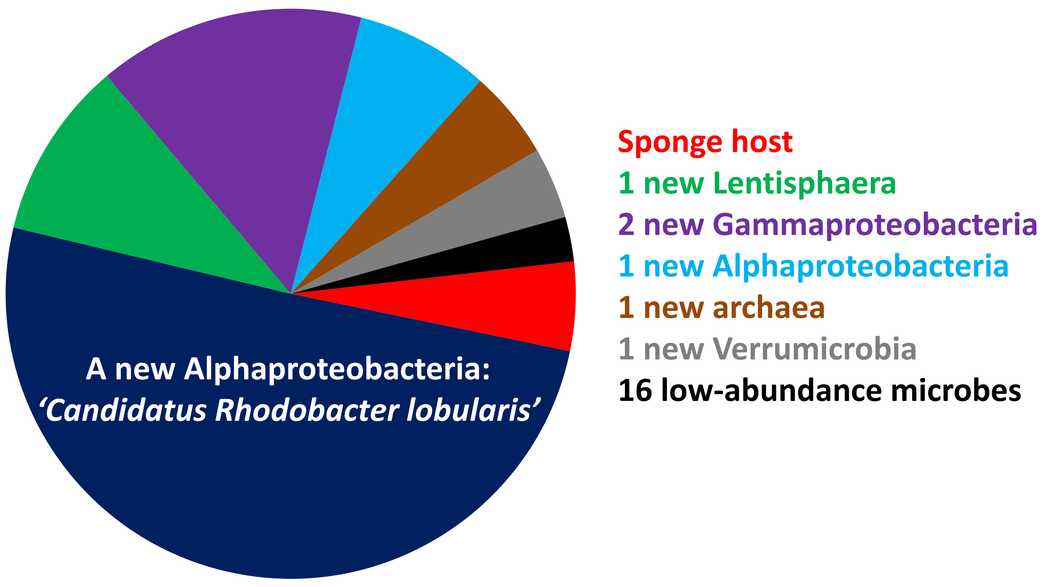
Distribution of size and GC% for genomic fragments (circles)

… of sponge genomes and more

Oopsacas minuta **metagenome composition**



Oscarella lobularis **metagenome composition**



Relative abundance compared to sponge host based on read mapping onto metagenome

CONCLUSIONS & PERSPECTIVES

- Metagenomics is a powerful tool to identify uncultured microorganisms such as symbionts.
- Metagenomics has revealed a high abundant microbe in each sponge.
- Analysis in progress: PacBio sequencing, comparative genomics, *in silico* reconstruction of metabolisms and Fluorescent *In Situ* Hybridization.

REFERENCE

Jourda, C., Santini, S., Rocher, C., Le Bivic, A., & Claverie, J. M. (2015). Draft genome sequence of an alphaproteobacterium associated with the Mediterranean sponge Oscarella lobularis. *Genome announcements*, *3*(5), e00977-15.